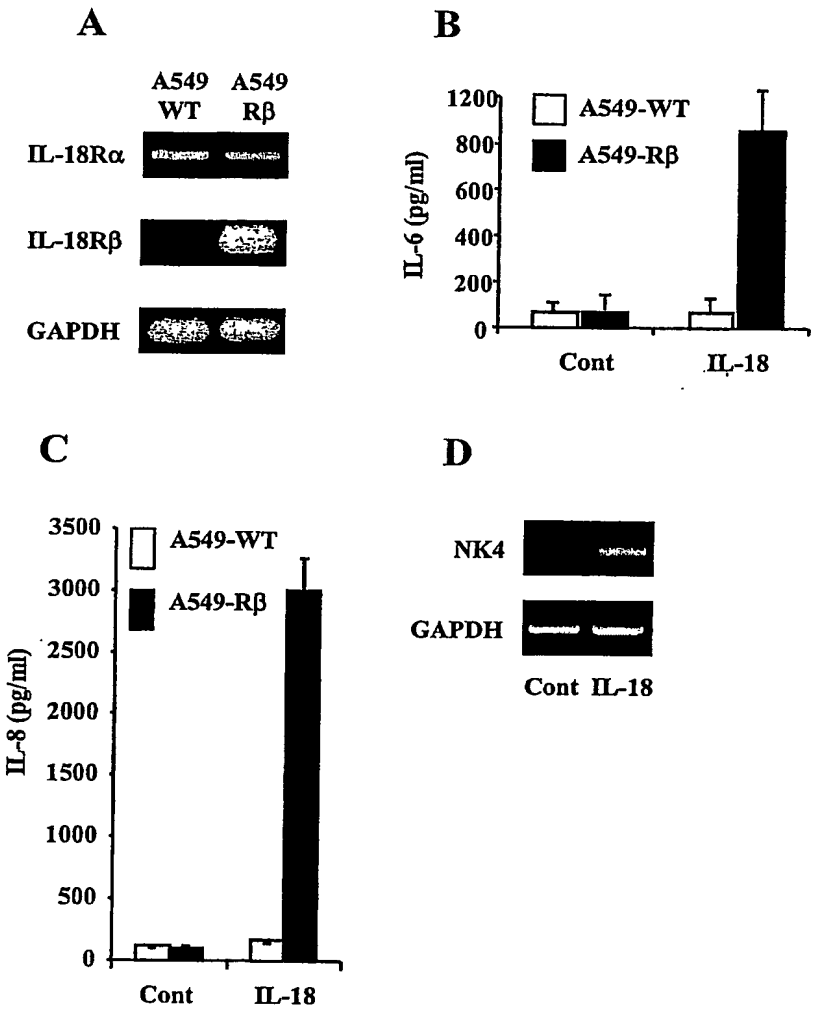

A
A549 WT
A549 Rβ
IL-18Rα
IL-18Rβ
GAPDH
B
1200
800
600
400
200
0
IL-6 (pg/ml)
A549-WT
A549-Rβ
Cont
IL-18
C
3500
3000
2500
2000
1500
1000
500
0
IL-8 (pg/ml)
A549-WT
A549-Rβ
Cont
IL-18
D
NK4
GAPDH
Cont IL-18

Fig. 1

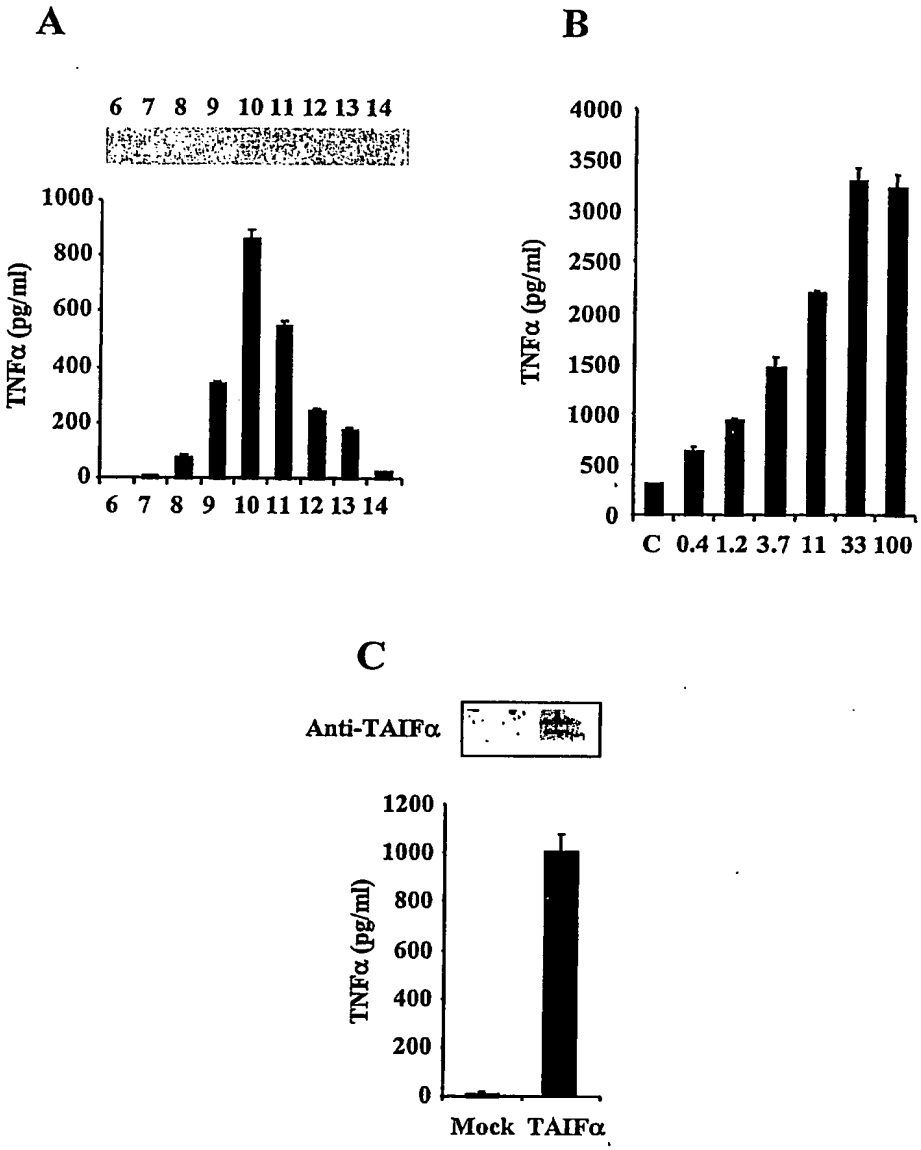

A
6 7 8 9 10 11 12 13 14
1000
800
600
400
200
0
TNFα (pg/ml)
6 7 8 9 10 11 12 13 14
B
4000
3500
3000
2500
2000
1500
1000
500
0
TNFα (pg/ml)
C 0.4 1.2 3.7 11 33 100
C
Anti-TAIFα
1200
1000
800
600
400
200
0
TNFα (pg/ml)
Mock TAIFα

Fig. 2

```
IL-32α      ATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAAGCTGAAGGCCCGAATG------
IL-32β      ATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAAGCTGAAGGCCCGAATG------
IL-32γ      ATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAAGCTGAAGGCCCGAATGGTAATG
IL-32δ      ----------------------------ATGAAGAAGCTGAAGGCCCGAATG------

IL-32α      ------------------------------------------------------------
IL-32β      ------------------------------------------------------------
IL-32γ      CTCCTCCCTACTTCTGCTCAGGGGTTGGGGGCCTGGGTCTCAGCGTGTGACACTGAGGAC
IL-32δ      ------------------------------------------------------------

IL-32α      ------------------------------------------------------------
IL-32β      ------------------------------------------------------------
IL-32γ      ACTGTGGGACACCTGGGACCCTGGAGGGACAAGGATCCGGCCCTTTGGTGCCAACTCTGC
IL-32δ      ------------------------------------------------------------

IL-32α      ------------CACCAGGCTATAGAAAGATTTTATGATAAAATGCAAAATGCAGAATCA
IL-32β      ------------CACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAATCA
IL-32γ      CTCTCTTCACAGCACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAATCA
IL-32δ      ------------CACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAATCA

IL-32α      GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32β      GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32γ      GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32δ      GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC

IL-32α      CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32β      CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32γ      CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32δ      CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
```

Fig. 3A

```
IL-32α      AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCTGTCCCGGATGTTGAGGAT
IL-32β      AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCTGTCCCGGATGTTGAGGAT
IL-32γ      AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCTGTCCCGGATGTTGAGGAT
IL-32δ      AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCCTGTCCCGGATGTTGAGGAT

IL-32α      CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAG----------
IL-32β      CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAGGTCATGAGATGGTTCCAGGCC
IL-32γ      CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAGGTCATGAGATGGTTCCAGGCC
IL-32δ      CCCGCAACCGAGGAGCCTGGGGAGAGCTTTTGTGACAAGGTCATGAGATGGTTCCAGGCC

IL-32α      ----------
IL-32β      ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGGTTCTGGCCTGGGTGAAGGAGAAGGTG
IL-32γ      ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGGTTCTGGCCTGGGTGAAGGAGAAGGTG
IL-32δ      ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGGTTCTGGCCTGGGTGAAGGAGAAGGTG

IL-32α      ----------
IL-32β      GTGGCCCTGGTCCATGCAGTGCAGGCCCTCTGGAAACAGTTCCAGAGTTTCTGCTGCTCT
IL-32γ      GTGGCCCTGGTCCATGCAGTGCAGGCCCTCTGGAAACAGTTCCAGAGTTTCTGCTGCTCT
IL-32δ      GTGGCCCTGGTCCATGCAGTGCAGGCCCTCTGGAAACAGTTCCAGAGTTTCTGCTGCTCT

IL-32α      ----------TCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32β      CTGTCAGAGCTCTTCATGTCCTCTTTCCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32γ      CTGTCAGAGCTCTTCATGTCCTCTTTCCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32δ      CTGTCAGAGCTCTTCATGTCCTCTTTCCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG

IL-32α      GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
IL-32β      GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
IL-32γ      GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
IL-32δ      GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
```

Fig. 3B

A

```
                1                                Myr
IL-32α          MCFPKVLSDDMKKLKARM----------------------------------------
IL-32β          MCFPKVLSDDMKKLKARM----------------------------------------
IL-32γ          MCFPKVLSDDMKKLKARMVMLLPTSAQGLGAWVSACDTEDTVGHLGPWRDKDPALWCQLC
IL-32δ          ----------MKKLKARM----------------------------------------

               61                        Myr
IL-32α          ----HQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPLLE
IL-32β          ----HQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPLLE
IL-32γ          LSSQHQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPLLE
IL-32δ          ----HQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPLLE

               121       Gly
IL-32α          KERDGLRCRGNRSPVPDVEDPATEEPGESFCDK--------------------------
IL-32β          KERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAWVKEKV
IL-32γ          KERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAWVKEKV
IL-32δ          KERDGLRCRGNRSPVPDVEDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAWVKEKV

               181                              Myr
IL-32α          ------------------------------SYGAPRGDKEELTPQKCSEPQSSK
IL-32β          VALVHAVQALWKQFQSFCCSLSELFMSSFQSYGAPRGDKEELTPQKCSEPQSSK
IL-32γ          VALVHAVQALWKQFQSFCCSLSELFMSSFQSYGAPRGDKEELTPQKCSEPQSSK
IL-32δ          VALVHAVQALWKQFQSFCCSLSELFMSSFQSYGAPRGDKEELTPQKCSEPQSSK
```

B

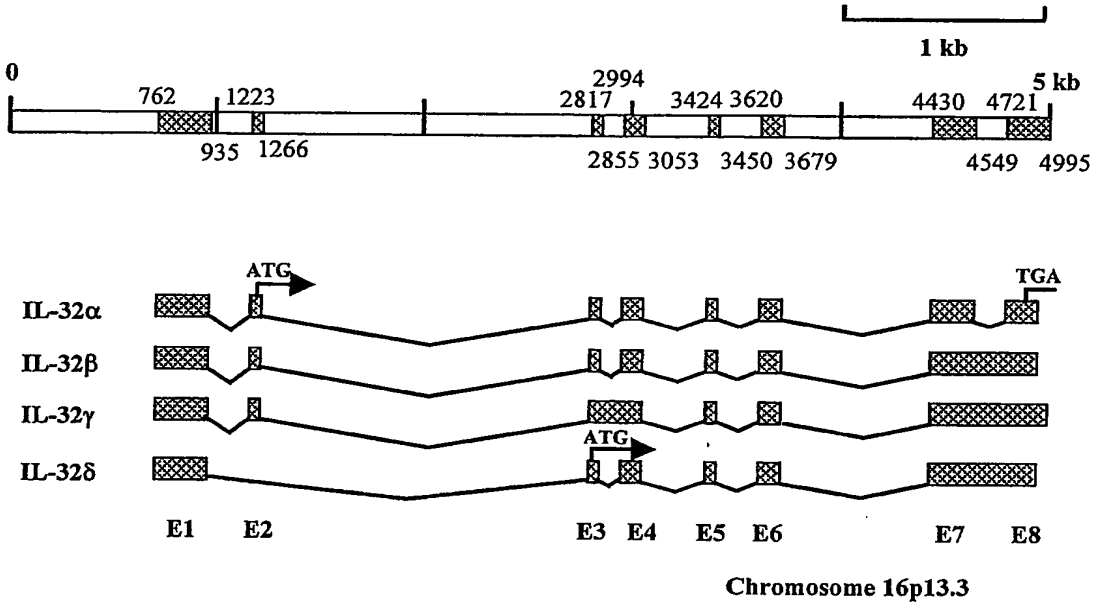
```
                1
huIL-32β        MCFPKVLSDDMKKLKARMHQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAA
EqIL-32         MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEEQVDLGLEDLEEKFSENILDAVEE
BoIL-32         MCFAKGVPYDQASLRSIMHKRVDDFCDKMGNEPE-EAQMEAALDETEEGLSEDICEFIED
Consensus       *---*----*----------------*---------------*---*----*--------

               61
huIL-32β        YYEEQHPELTPLLEKERDGLRCRGNRSPV----PDVEDP----ATE--EPGESFCDKVMR
EqIL-32         HHQKNNSESAPLLPDVKPRLRRRAQKSSVLNPEPEGPGILQVEALEAPEPEESFWVRAWR
BoIL-32         HIQENLPES--LQESSPL-LQEARQGVRRRIQRPSV-----SARLEVQNPEESI----WA
Consensus       -------*---*-------*-------------*-----------*---*-**------*-

               121
huIL-32β        WFQAMLQR-L-QTWWHGVLAWVKEKVVA------LVHAVQALWKQFQS---FCCSLSELF
EqIL-32         SFMGMLQR-LKQRWQAVLA-WVREKVAAGWQA--LCSVAQSINSVLES---FCSYMAGLF
BoIL-32         RALGRFQVIL-QSLQQRC--WDALTWLREKAVTFLEAICSVVKAVLGVLTDFCSSVGQLF
Consensus       ------*--*-*--------*-------------*----------------**------**

               181
huIL-32β        MSSF---QSYGAPRGDKEELTPQKCSEPQSSK
EqIL-32         RYH---IQV-----------------------
BoIL-32         ---GNLIQV-----------------------
Consensus       -------*-----------------------
```

Fig. 4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762
1223
2994
2817
3424 3620
4430 4721
5 kb
935 1266
2855 3053 3450 3679
4549 4995
ATG
TGA
IL-32α
IL-32β
IL-32γ
ATG
IL-32δ
E1 E2 E3 E4 E5 E6 E7 E8
Chromosome 16p13.3

Fig. 5

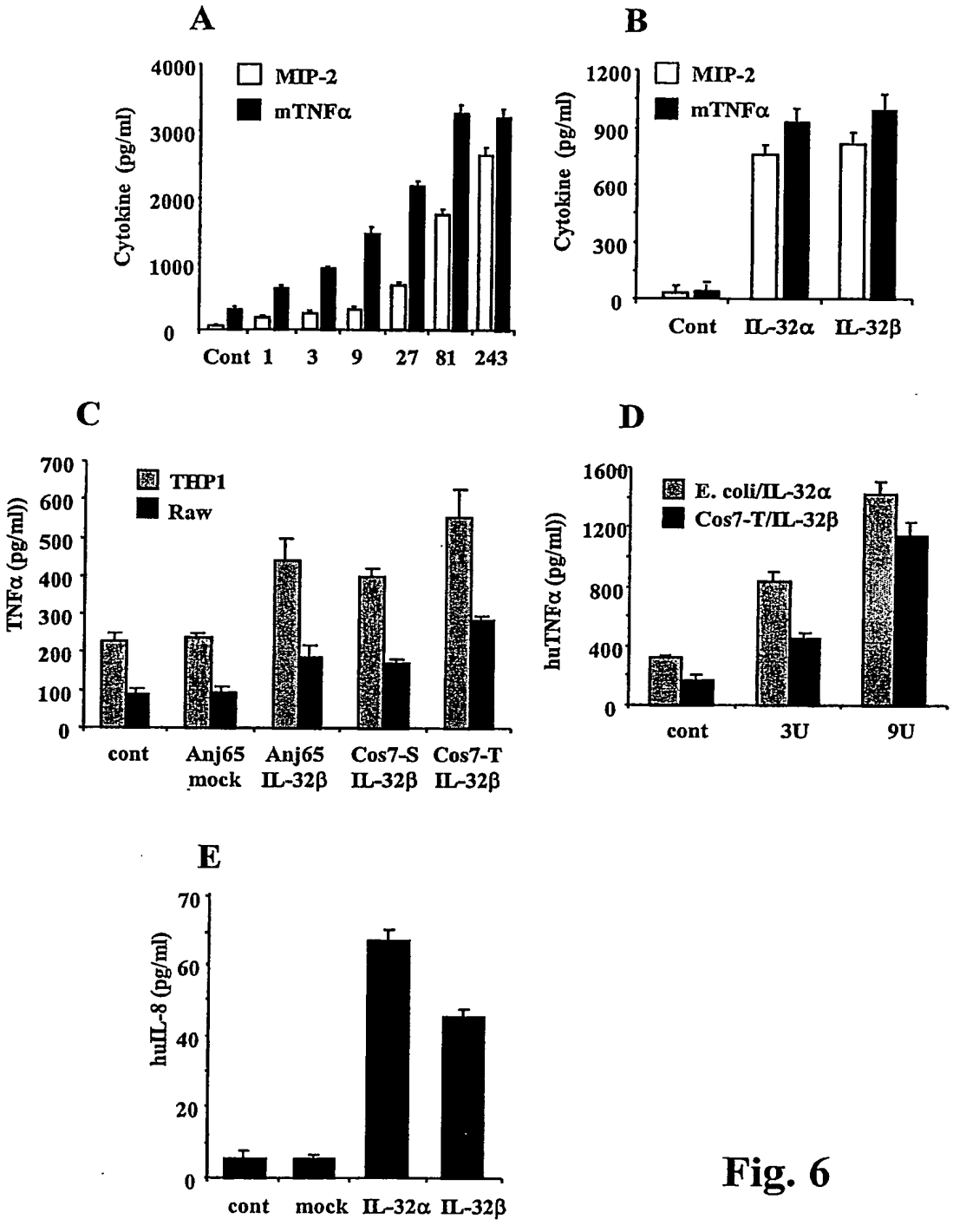
A
MIP-2
mTNFα
Cytokine (pg/ml)
4000
3000
2000
1000
0
Cont 1 3 9 27 81 243
B
MIP-2
mTNFα
Cytokine (pg/ml)
1200
900
600
300
0
Cont IL-32α IL-32β
C
THP1
Raw
TNFα (pg/ml))
700
600
500
400
300
200
100
0
cont Anj65 mock Anj65 IL-32β Cos7-S IL-32β Cos7-T IL-32β
D
E. coli/IL-32α
Cos7-T/IL-32β
huTNFα (pg/ml))
1600
1200
800
400
0
cont 3U 9U
E
huIL-8 (pg/ml)
70
60
40
20
0
cont mock IL-32α IL-32β

Fig. 6

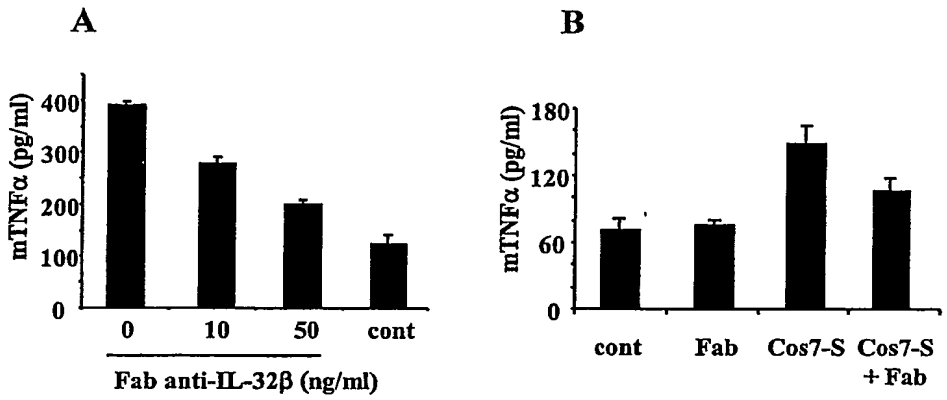
A
mTNFα (pg/ml)
400
300
200
100
0
0
10
50
cont
Fab anti-IL-32β (ng/ml)
B
mTNFα (pg/ml)
180
120
60
0
cont
Fab
Cos7-S
Cos7-S + Fab

Fig. 7

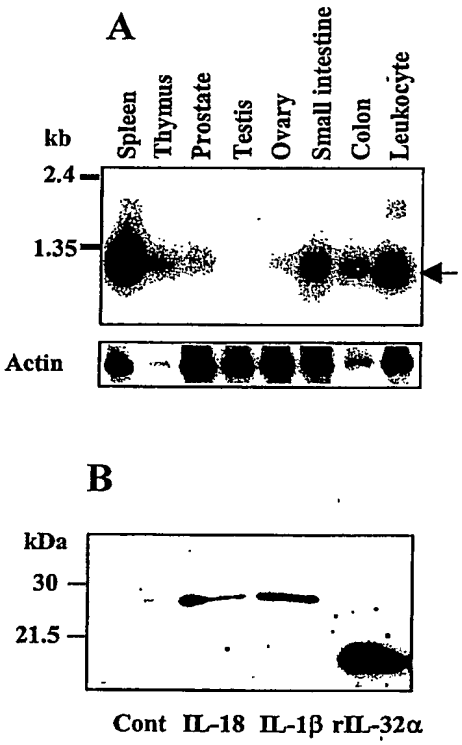
A
Spleen
Thymus
Prostate
Testis
Ovary
Small intestine
Colon
Leukocyte
kb
2.4
1.35
Actin
B
kDa
30
21.5
Cont
IL-18
IL-1β
rIL-32α

Fig. 8

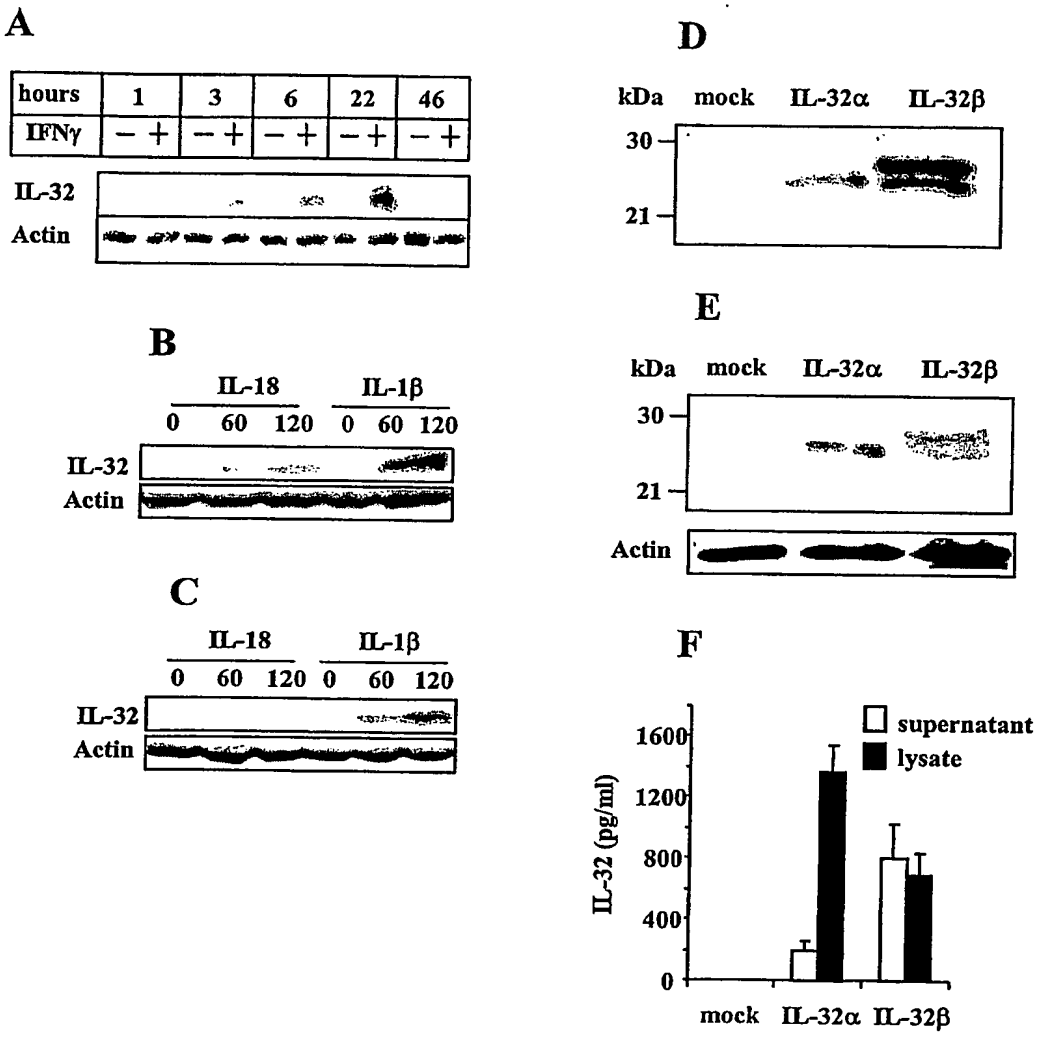
A
hours 1 3 6 22 46
IFNγ − + − + − + − + − +
IL-32
Actin
B
IL-18 IL-1β
0 60 120 0 60 120
IL-32
Actin
C
IL-18 IL-1β
0 60 120 0 60 120
IL-32
Actin
D
kDa mock IL-32α IL-32β
30
21
E
kDa mock IL-32α IL-32β
30
21
Actin
F
supernatant
lysate
IL-32 (pg/ml)
1600
1200
800
400
0
mock IL-32α IL-32β

Fig. 9

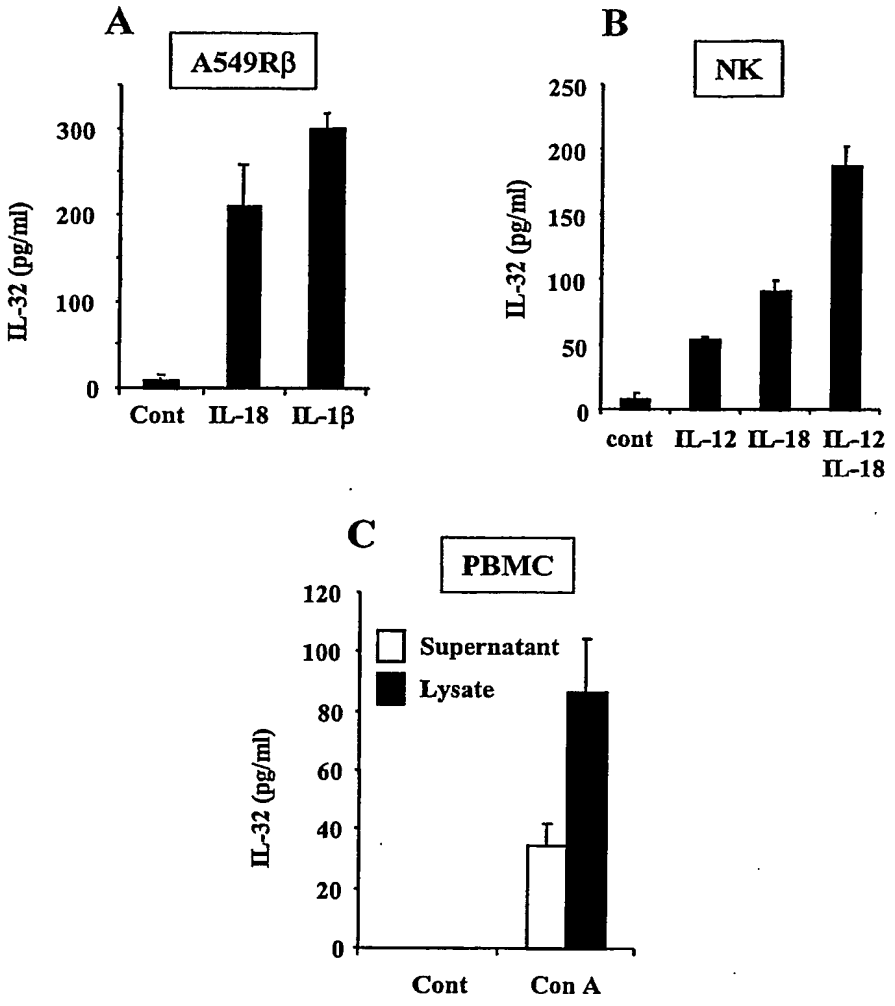
A
A549Rβ
IL-32 (pg/ml)
300
200
100
0
Cont
IL-18
IL-1β
B
NK
IL-32 (pg/ml)
250
200
150
100
50
0
cont
IL-12
IL-18
IL-12
IL-18
C
PBMC
IL-32 (pg/ml)
120
100
80
60
40
20
0
Supernatant
Lysate
Cont
Con A

Fig. 10

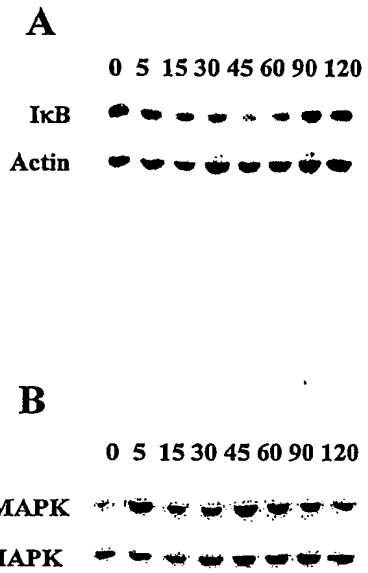
A
0 5 15 30 45 60 90 120
IκB
Actin
B
0 5 15 30 45 60 90 120
Ⓟ-p38 MAPK
p38 MAPK

Fig. 11

A

EqIL-32 alpha (SEQ ID NO:18)

MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEEQVCQCAPTPCSRNLGGRVVTMTMRRKNVPPQVD
LGPLTSPFSQRTFRSDLCHLPTLDLSLTTSLTSLLCTAWPPCPPCTSCSGFLLQV

B

EqIL-32 alpha (SEQ ID NO:19)

GCACGAGCTCGTGCCGTGTGCTGAGAGGCCCTTGGGGCAGGCACAGCCCCTGGAATCCTGAGCTGCCATG
GGCTACCCCAAGACGTCCAGAGAAGACAATGAACGTTGGAAGATCCGATTTCACAGCACTTTAGACCGGT
GGCTTGATGATATCGAAGTTCAATCCCAAGGAGAGGAACAGGTGTGTCAGTGTGCTCCCACGCCCTGCTC
CCGTAACCTCGGGGGTCGGGTGGTCACGATGACGATGAGGAGGAAGAACGTGCCACCTCAGGTCGATTTA
GGCCCTTTGACGTCCCCCTTTTCACAGAGAACCTTCAGAAGTGACCTTTGCCACCTGCCTACCCTTGACC
TGTCCTTGACCACCTCCCTCACCTCCTTGCTGTGCACAGCCTGGCCACCCTGCCCACCATGCACTTCCTG
CTCAGGTTTCCTTCTGCAGGTCTGACTTGTGGCTCCAGCGCATATGTCTTAATAAAGTTGTG

C

EqIL-32 beta (SEQ ID NO:16)

MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEEQVDLGLEDLEEKFSENILDAVEEHHQKNNSESA
PLLPDVKPRLRRRAQKSSVLNPEPEGPGILQVEALEAPEPEESFWVRAWRSFMGMLQRLKQRWQAVLAWV
REKVAAGWQALCSVAQSINSVLESFCSYMAGLFRYHIQV

D

EqIL-32 beta (SEQ ID NO:20)

CTGAGAGGCCCTTGGGGCAGGCACAGCCCCTGGAATCCTGAGCTGCCATGGGCTACCCCAAGACGTCCAG
AGAAGACAATGAACGTTGGAAGATCCGATTTCACAGCACTTTAGACCGGTGGCTTGATGATATCGAAGTT
CAATCCCAAGGAGAGGAACAGGTCGATTTAGGCCTAGAAGACCTGGAGGAAAAATTCAGTGAAAACATTC
TTGACGCCGTGGAGGAGCACCATCAGAAGAACAACTCAGAATCTGCGCCTTTACTTCCTGACGTGAAGCC
CAGGTTACGTCGCAGAGCTCAGAAGTCCTCTGTCCTCAACCCTGAACCTGAGGGTCCAGGGATCCTGCAA
GTTGAGGCTCTAGAGGCACCCGAGCCTGAAGAAAGCTTTTGGGTCAGAGCATGGAGGTCGTTCATGGGGA
TGCTACAGCGACTGAAGCAGAGGTGGCAGGCTGTACTGGCCTGGGTGCGAGAGAAGGTGGCTGCTGGCTG
GCAGGCCCTATGCAGTGTGGCCCAGTCCATTAATAGTGTGCTTGAGAGTTTCTGCTCCTATATGGCTGGG
TTGTTTAGGTACCACATCCAGGTCTAGGGGGCCCCATGGGGTCCAGGAGGGGTAGCCACACCTTGCAGCC
CTTTGACGTCCCCCTTTTCACAGAGAACCTTCAGAAGTGACCTTTGCCACCTGCCTACCCTTGACCTGTC
CTTGACCACCTCCCTCACCTCCTTGCTGTGCACAGCCTGGCCACCCTGCCCACCATGCACTTCCTGCTCA
GGTTTCCTTCTGCAGGTCTGACTTGTGGCTCCAGCGCATAGTCTT

Fig. 12

A

BoIL-32 beta (SEQ ID NO:17)

MCFAKGVPYDQASLRSIMHKRVDDFCDKMGNEPEEAQMEAALDETEEGLSEDICEFIEDHIQENLPESLQ
ESSPLLQEARQGVRRRIQRPSVSARLEVQNPEESIWARALGRFQVILQSLQQRCWDALTWLREKAVTFLE
AICSVVKAVLGVLTDFCSSVGQLFGNLIQV

B

BoIL-32 beta (SEQ ID NO:21)

CGGATTCCCGGGATGCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGGTCCCTTCGGGAGGACCCTAAGCC
ACCATGTGCTTCGCTAAGGGAGTCCCATATGACCAGGCTTCTCTGAGGTCCATAATGCACAAACGGGTGG
ATGATTTCTGTGATAAGATGGGAAATGAACCAGAAGAAGCACAGATGGAGGCAGCCCTAGATGAGACGGA
GGAGGGACTCAGCGAGGACATCTGTGAATTCATAGAAGATCACATTCAAGAGAACCTTCCCGAATCCCTG
CAGGAGTCCAGTCCCTTGCTTCAGGAAGCACGGCAAGGAGTACGCCGCAGAATCCAGAGACCTTCAGTCT
CTGCCCGTCTGGAGGTCCAGAATCCGGAAGAGAGCATCTGGGCCAGAGCCCTGGGGAGGTTCCAAGTAAT
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TCTTCGGAAACCTCATCCAGGTCTAGGAGCCGCAGGTGGTTCTGGAGGAACTCCTCCTCATCTAGGAGGC
CCTGCACCATCCCCTTCCCAGAAACCATCTTGTGAAGCGACCTTTGCACTCCTGCTCACCCTTGACCCAT
CCTTTAACTGCCCTCACCTCCTGT

C

BoIL-32 gamma (SEQ ID NO:22)

MCFTKRDPRVLASFRVLMVRSSFPRIAGVREAWVLLGEAENILAHLGPSREKNRDSFTQVHLCSQHNLVD
EFFDTMENEPEGAQMEAVLAETKEKFIKDAFKVMDNHIQENSPETLKESSPLLQEARQEVRCRIQRRSVS
TSLEVQNPEESIWARALRQFLGILQSFLSGCRDALTWLWEKAAACLQAICSAVEALWEVLTDFCSFVGQL
LCRSLIQV

D

BoIL-32 gamma (SEQ ID NO:23)

CGGGATCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGGTCCCAGCGGCAGGACCCTAAGCCACCATGTGC
TTCACTAAGAGAGACCCACGTGTCCTGGCTTCTTTCAGGGTGTTAATGGTAAGAAGCTCATTTCCACGTA
TAGCTGGGGTTCGGGAGGCCTGGGTTCTGCTGGGTGAAGCTGAGAACATTCTGGCCCACTTGGGACCCAG
CAGGGAGAAGAACCGAGATTCTTTTACTCAAGTCCATCTCTGTTCACAGCACAACCTTGTAGATGAATTT
TTCGATACAATGGAAAATGAACCAGAAGGAGCACAGATGGAGGCAGTCCTAGCAGAGACTAAGGAGAAAT
TCATCAAGGACGCCTTTAAAGTCATGGATAATCACATTCAAGAGAACAGTCCCGAAACCCTGAAGGAGTC
CAGTCCCTTGCTTCAGGAAGCACGGCAAGAAGTACGCTGCAGAATCCAGAGACGCTCCGTCTCCACCTCT
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CTGCAGTGCGGTGGAGGCCCTCTGGGAAGTGCTCACGGATTTCTGCTCCTTTGTTGGGCAGCTCTTATGC
AGAAGCCTCATCCAGGTCTAAGAGCCTCACATGGTTCTGGAGGAGCCCCACCTCATTCAGAAGGCCCTGT
ACGATGCCCTTCCCGGAAACCATCTTCTGAAGCGACCTTTACCCTCCTGCTCACCCTTGACCCATCCTTT
AACTGCCCTCCCCTCCTGTCCTG

Fig. 13

A

OvIL-32 alpha (SEQ ID NO:24)

MCFARGVPHDQASLRSMLHTWVDHVCDKMGNEPEEAQMEAALAEMEEELSKDVCESWKITFKRTFPNPCR
SPVPCFRKRSKKYAAESRDPQSLPVWRTRNRKRASGPEPCGGSEVFCGVSGSGVAMY

B

OvIL-32 alpha (SEQ IDO:25)

CTGCGGTACCGGTCCGGATTCCCGGGCGAGACAGTGCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGATC
CCAGCCGGAGGACCCTAATCCACCATGTGCTTCGCTAGGGGAGTCCCACATGACCAGGCTTCTCTGAGGA
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GGCAGCCCTAGCAGAGATGGAGGAGGAACTCAGCAAGGATGTCTGTGAATCATGGAAGATCACATTCAAG
AGAACCTTCCCGAATCCCTGCAGGAGTCCAGTCCCTTGCTTCAGGAAGCGCAGCAAGAAGTACGCCGCAG
AATCCAGAGACCCTCAGTCTCTGCCTGTCTGGAGGACCAGAAACCGGAAGAGAGCATCTGGGCCAGAGCC
CTGCGGCGGTTCCGAGGTTTTCTGCGGAGTCTCTGGCAGCGGTGTTGCGATGTACTGACCTGGCTGCAGG
AGAAGGCGGCGGCCTGCCTGGAGGCCGTCTGCAGTGCGGTGAAGACCATCTGGGGAGTGCTGACGGATTT
CTGCTCCTCTGTGGGGCAGCTCTTCAGAAACCTCATCCAGGTCTAGGAGCCCCAGGTCGTTCTTGAGGAA
CTGCTCCTCATCTAGAAGGCCCTGCACAATCCCCTTCCCAGAAACCATCTTCTGAAGCGACCTTTACCCT
CCTGTTCACCCTTCACCAATCCTTTAACTGCCCTCACCTCCTGTCTGCAGGGACGACACCACAACATCAA
GCCAGGTTTCCCTTCTCCAAGTCTGACCCGTCTGTCAGGGA

C

SwIL-32 alpha (SEQ ID NO:26)

MRGVSATRTLPKAGPQPRSGLGLPLPRRVPEPPPIPAESSPLLNEVRQGVRSRVRRPPGHNQPHYALAVR
EPRQSTFRRILELFEEMLKRLQQRWRGALAWVQERAAACFRGLCRALEAFWSLVQSFCSSMGHAFGSVIQ
V

D

SwIL-32 alpha (SEQ ID NO:27)

ATGACTTGGAGGGGAACTGAGCGGCCAGGCCCAGCCCCTGGGAAAAGTCCTGGGGTCTGTGGGGCTGTTG
GCAGGAAAGCAGCCTGTGTCCAAGGCGGGGCATGAGGGGGGTGTCTGCCACCAGGACTCTCCCAAAGGCA
GGGCCTCAGCCAAGGTCAGGACTGGGGCTGCCTCTCCCCAGGCGGGTCCCTGAACCACCCCCCATCCCTG
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CAACCAGCCACATTATGCGCTAGCGGTCCGGGAGCCCAGGCAGAGCACTTTCAGACGCATCCTTGAGCTG
TTTGAGGAAATGCTGAAGCGCCTGCAGCAGAGGTGGAGGGGTGCCCTGGCTTGGGTGCAGGAAAGGGCTG
CTGCCTGCTTCCGGGGCTTGTGCAGGGCCCTTGAAGCTTTCTGGAGCCTGGTGCAGAGTTTTTGCTCCTC
CATGGGGCACGCCTTCGGGAGTGTCATCCAGGTCTAAGGTGCTCCAGGTGAAATAAGAGTTTCTAGAGCA
CAACCTCCCCCTGCCTTGGCTAAAAAGGCAGCTGTAAGCCTTT

Fig. 14